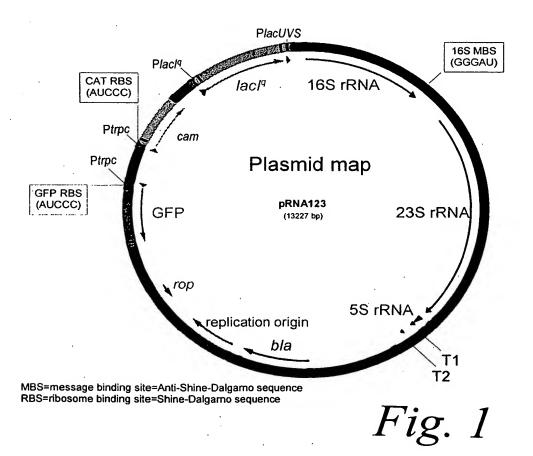
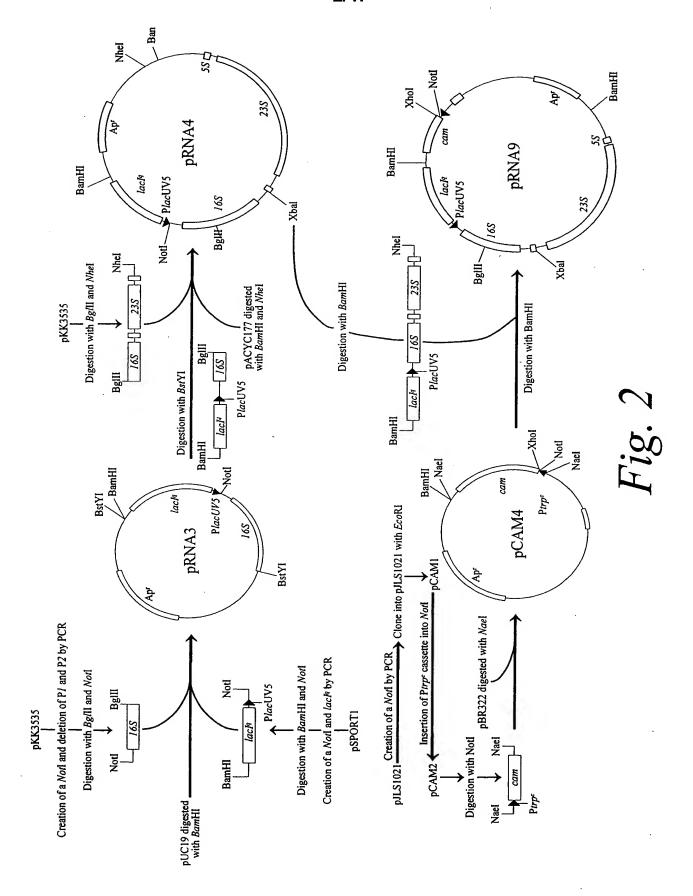


1/47

Necleotide	Description
1-1542	16S rRNA of Escherichia coli rrnB operon
1536-1540	16S MBS (message binding sequence) GGGAU
1543-1982	16S-23S spacer region
1983-4886	23S rRNA of Escherichia coli rrnB operon
4887-4982	23S-5S spacer region
4983-5098	5S rRNA of Escherichia coli rmB operon
5102-5145	terminator T1 of Escherichia coli rrnB operon
5276-5305	terminator T2 of Escherichia coli rrnB operon
6575-7432	bla (β-lactamase; ampicillin resistance)
7575-8209	replication origin
8813-8622	rop (Rop protein)
10201-9467	GFP (Green Fluorescent Protein)
10213-10209	GFP RBS (ribosome binding sequence) AUCCC
10270-10230	trpc promoter
10745-10785	trpc promoter
10802-10806	CAT RBS (ribosome binding sequence) AUCCC
10814-11473	cam (chloramphemcol acetyltransferase: CAT)
11782-11859	<i>lac^q</i> promoter
11860-12942	lacl ^q (lac repressor)
12985-13026	lacUV5 promoter





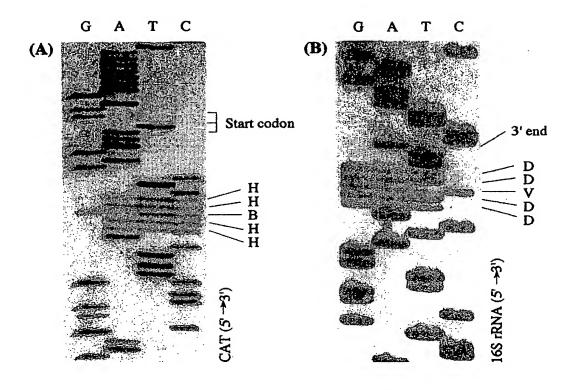


Fig. 3

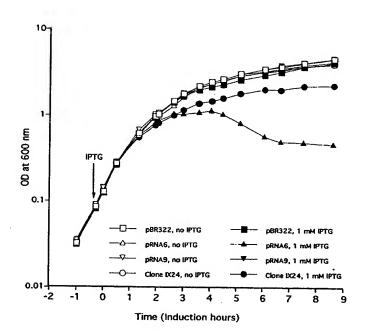
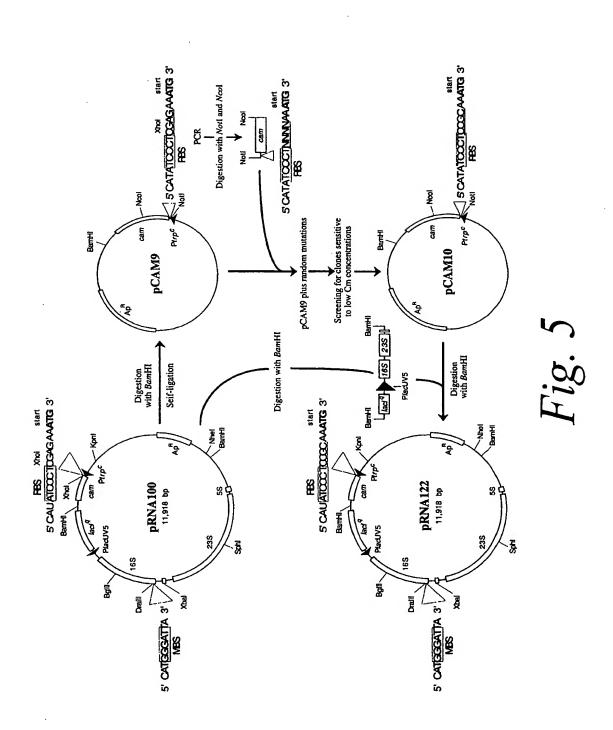


Fig. 4

:)



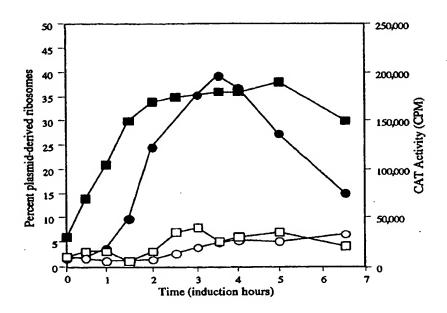


Fig. 6

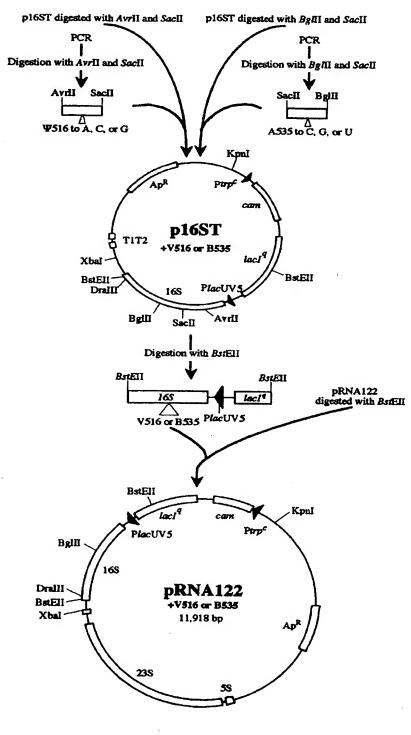


Fig. 7

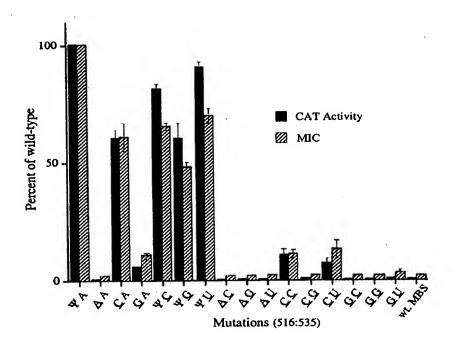


Fig. 8

Oligo	Sequence (5' to 3')	Used for
기 기 기	ATAGGGGTTCCGCGCACATT CTCGAGCCTCCTGAAAGCGGCCG CAACTCAAAAAATACGCCCGGT	Primer cam from268 to249 Creating a Notl in the upstream of cam
OR2 IR2	AAATCGTCGTGGTATTCACT GCGGCCGCTTTCAGGAGGCTCGA	Primer cam from 473 to 492 Creating a Notl in the upstream of cam
TRP'-T	GAAATGGAGAAAAAN LALI GGCGGCTAGCCGGCGAGCTGTTG ACAATTAATCATCGAACTAGTT	Promoter <i>trpc</i> , top strand
TRP'-B	TAATGTGTGGAAGC GGCCGCTTCCACATTAAACTA GTTCGATGATTAATTGTCAACAG	Promoter <i>trpc</i> , bottom strand
SD*-B SD*-T lacU	TCGAGCACAGAGC GGGCACTTCAGTGTGC GGTCATAGGCGGCCGCTGTGGA AATTGTTATCCGCTCACAATTCC	Mutated RBS for pCAM5; top strand Mutated RBS for pCAM5; bottom strand Creating a Notl and PlacUV5 mutation in the 3' end of lacl
lact	ACACA I A I A CGAGGCAAAGC TTGGATCCGACACCATCGAATGG	Creating a BamHI and lacl9 mutation in the 5' end of lacl
01.4	GAAGGATCCGCCGAAGATGTTT	Primer 16S rRNA from -707 to -689; creating a BarnHI in the 5'
1.4	GCGCCGCTTAAAATAATTTTCT	Primer 16S rRNA from -351 to -333, deleting P1P2 and creating a Nort in the 5' end of 16S rRNA
OR4	CCACAAGCTTCGCACCTGAGCGT	Primer 185 RNA from 745 to 765; creating a Hindlil in the middle of 16S rRNA
IR4	AAAATTATTTAAGCGGCCGCTG AGAAAAAGCGAAGC	Primer 16S rRNA from -164 to -180; deleting P1P2 and creating a Nort in the 5' end of 16S rRNA
ASD*-B ASD*-T	GGCGACTITCACTCACAAAC GTCGAAGCTTGGTAACCGTAGGG GAACCTGCGGTTGGATCACACAC	Primer tRNAGlu from +8 to +27 Primer 16S from 1504 to +16, mutating the MBS region from C1536UC1538 to A1536CA1538
Cat-M-Xhol	TTAATGTGTGGAAGCGGCCGCTT TCATATCCCTNNNNAAATGGAG	Primer cam from -39 to +15; creating 4 nucleotide random mutations
Cat-N-Ncol	CAGCACCTTGTCGCCTTGC	Primer cam from 688 to 706

č	Description	0	
Plasmid	Description	neierence	
pUC19	Cloning vector	(67)	
pBR322	Cloning vector	(62)	
pACYC177	Cloning vector	(72)	
pKK3535	pBR322 derivative containing Intact mB operon	(31)	
pSPORT1	pUC19 derivative containing faci	(57)	
DLS1021	pBR322 derivative containing cam	(28)	
pSTL102	pKK3535 containing U1192 in 16S rRNA and G2058 in 23S rRNA	(34)	
pCAM1	pJLS1021 plus a NotI site in the upstream of cam	This study	
pCAM2	pCAM1 plus Ptrpc between Notl sites in the upstream of cam	This study	
pCAM4	pBR322 plus the Nael fragment of pCAM2 containing cam under Ptrpc	This study	
pCAM5	pCAM4 containing RBS (5'-GUGUG) of Hul et al. (1) in cam	This study	
pCAM9	pCAM5 containing selected RBS (5'-AUCCC) in cam	This study	
pCAM10	pCAM9 containing selected upstream sequence of cam	This study	
pRNA3	pUC19 plus lacid and 5' end of 16S rRNA under PlacUV5	This study	
pRNA4	pACYC177 plus lacid and rmB with wild-type MBS under Plac UV5	This study	
pRNA5	pRNA4 containing MBS (5'-CACAC) of Hui et al. (1) in 16S rRNA	This study	
pRNA6	pCAM5 plus the BamHI fragment containing lacid and rmB from pRNA5	This study	
pRNA8	pCAM5 plus the BamHI fragment containing lacid and rmB from pRNA4	This study	
pRNA9	pCAM4 plus the BamHI fragment containing lacid and rmB from pRNA4	This study	
pRNA100	pRNA8 containing selected MBS (5'-GGGAU) and RBS (5'-AUCCC)	This study	
pRNA101	pRNA100 containing U1192 in 16S rRNA	This study	
pRNA104	pRNA101 containing U2058 in 23S rRNA	This study	
p16ST	pUC19 derivative containing cam, lacid and 16S rRNA from pRNA100	This study	
pRNA122	pRNA100 containing selected upstream sequence of cam from pCAM10	This study	
pRNA170	pRNA122 containing U1192 in 16S rRNA and U2058 in 23S rRNA	This study	
			١

MIC with no induction 50 100	0 200	400	500	009	700	800	1000
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Clone	RNA sequences	∆G 37	MIC	ا ن	5	CAI	Induction
	5' C A R1 R2 R3 R4 R5 C U C G 3' CAT mRNA		µg of Cm∕ mL	of Cm/ mL	0	СРМ	
Random	3' A U U MS M4 M3 M2 M1 A C U S' 16S FRNA	kcal/mol	7	Ŧ	T	Ŧ	-1/+1
pRNA9	5, C A <u>G G A G G</u> C U C G 3' 3' A U U <u>C C U C G</u> A C U 5'	-9.8	200	200	2803 ± 68	2700 ± 196	1.0
pRNA6	5, C A G U G U G C U C G 3' 3' A U U C A C A G A C U 5'	-7.8	5	200	4033 ± 1040	12437 ± 2491	3.1
VII30	5, C A <u>U A U C C C U</u> C G 3' 3' A U U <u>U A G G G A</u> C U 5'	-8.4	100	200	6293 ± 706	72206 ± 706	11.5
VII43	5, C A A A C A C C U C G 3' 3' A U U G G A G A A C U 5'	-8.1	125	200	5603 ± 1011	47667 ± 891	8.5
VII64, VII65	5, C A <u>U A C C U</u> C U C G 3' 3' A U U <u>G G A G U</u> A C U 5'	-7.3	6	200	6200 ± 953	37311 ± 3978	6.0
VIII29	5' C A <u>U A A U C C U C</u> G 3' 3' A U U A <u>G G A G</u> A C U 5'	-10.9	125	009	7869 ± 416	91153 ± 4003	11.6
VIII46	5, C A A A U A C C U C G 3' 3' A U U G G A G U A C U 5'	-7.7	00	200	6431 ± 816	46840 ± 796	7.3
VIII77	5, C A <u>C A U A C C U C</u> G 3' 3'A U U <u>G G A G U</u> A C U 5'	-7.7	150	009	6794 ± 650	44358 ± 4841	6.5
VIII93	5, C A <u>C C G G C U C G 3'</u> 3' A U U <u>G G A G A</u> A C U 5'	-8.5	6	200	5643 ± 897	24888 ± 2388	4.4
1)24	5, C A <u>U A U C C</u> U C G 3' 3' A U U <u>A G G Q</u> U A C U 5'	-7.3	9	650	7524 ± 263	91809 ± 4542	12.7
IX32	5, C A <u>A C U A C C U C</u> G 3, 3, A U U <u>G G A G</u> U A C U	-7.7	001	200	5783 ± 971	32164 ± 5862	5.6
1X67	5' C A <u>U A U A C C U C</u> G 3' 3' A U U <u>G G A G</u> A A C U 5'	-8.0	125	009	6063 ± 787	24581 ± 3009	1.4

Clone	RNA sequences	MIC	O
	5' C A U A U C C C U N N N A A A U G 3' CAT mRNA	(Jm/g/mL)	mL)
positions	3'AUUAGGGUACUAGG5' 16S rRNA	Ŧ	7
pRNA100	5, C A U A U C C C U C G A G A A A U G 3' 3'A U U A G G G U A C U A G G 5'	100	059
pRNA100 + wt MBS	s, c a u a u c c c u <u>c c a c</u> a a a a u e s' 3' a u u c <u>c u c</u> c a c u a e e s'	20	20
pRNA122	s, c a u a u c c c u <u>c c c a c</u> a a a u e s' s' a u u a e e e u a c u a e e s'	20	009
pRNA122 + wt MBS	5, c A U A U C C C U <u>C G C</u> A A A U G 3′ 3′A U U C C U C C A C U A G G 5′	10	10
pRNA125	5, C A U A U C C C U <u>C C U G</u> A A A U G 3' 3'A U U A G G G U A C U A G G 5'	80	009
pRNA127	s, c a u <u>a u c c c u c c c a a a a u e s</u> , s, a u <u>u a e e e u</u> a c u a e e s,	90	900
pRNA128	5, C A U A U C C C U C C A C A A A U G 3, 3, A U U A G G G U A C U A G G 5,	20	009

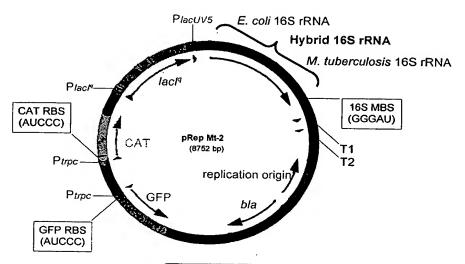
		Percent plasmid-derived 30S in	S.in	
Residue at 516	30S peak	70S peak	Crude ribosomes	% CAT
Ψ	46.5 ± 3.6	53.0 ± 4.5	47.8 ± 2.8	100
∢	54.2 ± 5.4	10.6 ± 1.4	37.5 ± 3.9	0
O	51.8 ± 0.2	27.1 ± 2.9	42.9 ± 5.8	59.4
o	67.5 ± 6	8.8 ± 0.9	44.1 ± 5.2	6.3

Clone	Alignment of CAT mRNA and 16S rRNA	ا io gم)	MIC (Cm/mL)	
Random	5' C A R1 R2 R3 R4 R5 C U C G 3' CAT mRNA 3' A U U M5 K4 M3 M2 M1 A C U 5' 165 rRNA	no IPTG	1 mM IPTG	ΔG <u>₹</u> - (kcal/mol)
wild-type	5' C A Q Q A Q Q C · U C Q 3' 3' A U U C C U C Q X C U 5'	500	500	-9.8
1	5'. C A A U C C C C C U C G 3' 3' A U U A Q Q Q A A C U 5'	100	400	-8.3
2	5' C A U A C C U C U C G 3' 3' A U U Q Q Q - U A A C U 5'	50	100	-4
3	5' C A C A Q U C C U C G 3' 3' A U U A Q C A Q A C U 5'	50	100	-1.9
4	5' C A A A C C A C U C G 3' 3' A U U U A Q U Q A C U 5'	50	100	-4.1
5	5' C A W A Q C C C U C G 3'	50	100	-7.6
6	5' C A H C H H C C U C G 3'	50	100	-7.4
7	5' C A A U U A U C U C G 3' 3' A U U U U A A Q A C U 5'	50	100	-3.1
8	5' C A Q A Q A A C U C G 3' 3' A U U Q A Q U A A C U 5'	100	200	-3.6
9	5' C A A A Q U U C U C G 3' 3' A U U Q A Q U A A C U 5'	100	200	-0.6
10	5' C A A U U C A C U C G 3' 3' A U U A A Q U Q A C U 5'	100	400	-7.7
11	5' C A A C U C A C U C Q 3' 3' A U U Q U G A Q A C U 5'	100	200	-7.1
12	5' C A A C C C A C U C G 3' 3' A U U A C C C U A C U 5'	50	100	-ė
13	5' C A Y C C Y U C U C C 3' 3' A U U C A Q A A A C U 5'	50	200	-2.2
14	5' C A Q A Q Q A C U C G 3' 3' A U U U U Q Q U A C U 5'	50	100	-4.7
15	5' C A Q Q Q A A A C U 5'	50	200	-7
16	5' C A U Q Q Q A C U C G 3' 3' A U U Q Q Q Q A A C U 5'	50	100	-7.3
17	5' C A A A C U C C U C G 3' 3' A U U A U C A U A C U 5'	50	100	0.8
18	5' C A U A C A U C U C G 3' 3' A U U U Q A Q A A C U 5'	50	100	-2.1
19	5' C A A C U C U C U C G 3' 3' A U U A Q A Q Q A O U 5'	50	200	-5.6
20	5' C A A A U A U C U C O 3'	200	500	-6.2
21	5' C A U A C C U C U C G 3' 3' A U U Q Q A Q U A C U 5'	200	500	-7.3
22	5' C A U A Q U A C U C Q 3' 3' A U U U A Q Q U A C U 5'	100	200	0.3
23	5' C A A U C C A C U C G 3'	200	400	-10.6
24	S' C A Q A Q A Q C U C Q 3'	100	200	-0.2

Fig. 15

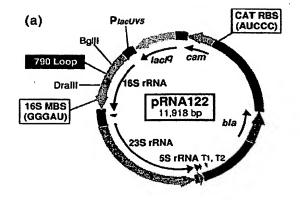
Clone	Alignment of CAT mRNA and 169 rRNA	(μg o	MIC f Cm/mL)	
Random	5' C A R1 R2 R3 R4 R5 C U C G 3' CAT mRNA 3' A U U K5 H4 K3 H2 N1 A C U 5' 165 rRNA	no IPTG	1 mM IPTG	4Gg7 (kcal/mol)
25	5' C A <u>U A Q C A</u> C U C G 3' 3' A U U A <u>U C Q U</u> A C U 5'	200	400	-6.8
26	5' C A A Q U A A C U C G 3' 3' A U U Q U G A U A C U 5'	100	200	-3.4
27	5' C A A A U A U C U C G 3' 3' A U U A U Q Q A A C U 5'	100	400	-5.3
28	5' C A A A U A Q A Q Q A C U 5'	200	400	-1.6
29	5'.C A C W C C W C U C G 3' 3' A U U A G Q A Q A C U 5'	50	100	-9.1
30	5' C A U A A Q Q U A C U 5'	100	400	-5.3
31	5' C A A C C U A C U C G 3' 3' A U U A Q A Q Q A C U 5'	50	200	-3.1
32	5' C A A U Q Q A C U C G 3'	100	400	-4.5
33	5' C A A C C C C C C C G 3' 3' A U U Q Q Q A Q A C U 5'	100	400	-7.2
34	5' C A A A Q A U C U C G 3' 3' A U U Q U A Q A A C U 5'	200	400	-8
35	5' C A U C C C A C U C Q 3' 3' A U U A U Q Q Q A C U 5'	50	200	-5
36	5' C A C U Q A U C U C G 3' 3' A U U A Q Q A G A C U 5'	200	500	-3.9
37	5' C A U A U Q Q C U C G 3' 3' A U U U A Q Q Q A C U 5'	100	500	-8.4
38	5' C A A A Q A Q C U C Q 3' 3' A U U Q Q A Q A A C U 5'	150	500	-8.1
39	5' C A A C Q A A C U C G 3' 3' A U U Q U Q A Q A C U 5'	100	400	-5.7
40	5' C A U C U A U C U C G 3' 3' A U U A Q A Q Q A C U 5'	100	400	-6.2
41	5' C A U A C C U C C 3' 3' A U U G Q A Q U A C U 5'	100	500	-7.3
42	5' C A U A U A A C U C G 3' 3' A U U A Q A Q A A C U 5'	200	500	-3.6
43	5' C A A A U A Q C U C Q 3' 3' A U U Q Q A Q U A C TU 5'	100	500	-7.7
44	5' C A C A U A C C U C G 3' 3' A U U Q Q A Q U A C U 5'	150	600	-7.7
45	5' C A Q Q Q A Q C U C Q 3' 3' A U U Q Q A Q A A C U 5'	100	500	-8.5
46	5' C A U A U C C C U C G 3' 3' A U U Q Q Q Q U A C U 5'	100	700	-7.3
47	5' C A A C U A C C U C Q 3' 3' A U U Q Q A Q U A C U 5'	100	500	-7.7
48	2, C Y A Y A G C A O O 2,	200	600	-8

Fig. 16



Nucleotide	Description
1-931	part of 16S rRNA from Escherichia coli rrnB operon
932-1542	part of 16S rRNA from Mycobacterium tuberculosis rrn operon
1536-1540	16S MBS (message binding sequence) GGGAU
1791-1834	terminator T1 of Escherichia coli rrnB operon
1965-1994	terminator T2 of Escherichia coli rrnB operon
3054-2438	replication origin
3214-4074	bla (β-lactamase; ampicillin resistance)
5726-4992	GFP (Green Fluorescent Protein)
5738-5734	GFP RBS (ribosome binding sequence) AUCCC
5795-5755	trpc promoter
6270-6310	trpc promoter
6327-6331	CAT RBS (ribosome binding sequence) AUCCC
6339-6998	cam (chloramphenicol acetyltransferase; CAT)
7307-7384	lacl ^q promoter
7385-8467	lacl ^q (lac repressor)
8510-8551	lacUV5 promoter

Fig. 17



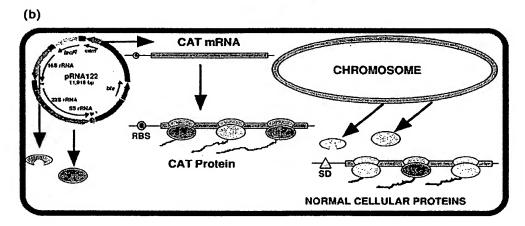


Fig. 18

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MIC* (µg/ml)	787	788	789	Nucle 790	eotide sequen 791	792	793	794	<i>7</i> 95	Number of mutations	Number of occurrences ^d
600°	A	U	U	A	G	A	U	A	С	0	WT
550 500	A A	ប ប	ប ប	A C	G G	GA	U C	A A	A	2 3	1
500	Α	Α	U	C Ā	G G G	Ğ	CID CID CIAID	Α	ğ	2	1
500 450	A A	. <u>Ā</u>	U U	A A	G	ç	C U	U Ā	C	4 1	1 1
450	Α	ŭ	U	<u>C</u> Ā	G	Ā	ç	Ä	č	2	1
450 450	A A	<u>C</u>	U U	A A	G G	<u>c</u>	₽	C U	<u>A</u>	5 3	1 1
450	Α	U CICIAIAIAIU	U	Α	G G	Ă	U	Ā	č	1	2
450 450	A A	A	ប ប	A C	G G G	ς υ	₽	U	C	4 5	1
450	G Ā	Ä	U	C Ā	Ğ	Ğ	ซื	Ā	<u>ū</u>	4	1
400 400	A A	A	บ บ	A A	G .	G	Ü	Ŭ	C	2 3 .	1 2
400 400	Α	<u>A</u> <u>A</u> <u>U</u>	Ü	Α	G	Ω̈́	<u>c</u>	Ā	A	4	2
350	A A		บ	<u>C</u>	0 0 0 0	Ä	Ā	A	A	5 2	1 1
350 350	A A	ប ប	U U	A A	G	Ë	Ğ	A	<u>c</u>	2 3	2 3
350	Α	U	U	Α	G	<u>c</u>	<u>C</u>	X	A	3	2
350 350	A A	ဋ	ប	A A	Ġ G	Ë	Ç	<u>U</u>	. <u>c</u>	4 3	2 2
350	Α	Ğ	U	Α	G	<u>Ğ</u>	<u>A</u>	<u>ŭ</u>	č	4	2 .
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Fig. 19

Nucleotide	787	788	789	790	791	792	793	794	795
A. Nucleotide d	istribution of	functional mi	ıtants ^a						
Α	<u>54</u>	24	0	69	0	15	18	35	16
C	2	16	0	<u>69</u> 8	Ō	15 24	26	<u>35</u> 5	
G	22	21	0	1	<u>78</u>	16	4	9	<u>34</u> 7
υ.	0	1 <i>7</i>	78	Ō	$\frac{1}{0}$	23	30	29	21
Consensus	R	<u>17</u> N	<u>78</u> U	M	Ğ	N	<u>30</u> H	· w	H
B. Nucleotide di	istribution in	all known bac	teria ^b						
A	573	0	0	578	1	578	n	577	0
C	3	0	0	0	î	2/0	ň	3//	- U
G	1	0	Ō	ŏ	576	ň	3	ņ	<u>578</u>
IJ	1	<u>578</u>	578	Ď	<u>576</u> 0	ň	575	0	0
Consensus	A	Ū	U	Å	Ğ	Ă	<u>575</u> U	Ä	Č
C. Nucleotide di	istribution in	all known org	anisms ^e						
A	1657	2 °	1	1648	2	1655	5	1664	- 1
3	6	1	566	9	ĩ	1	12	1004	1665
3	4	0	Ó	3	1662	7	46	2	1665
J	1	1664	1101	7	3	3	1605	1	0
Δ	0	1	0	í	ő	2	1003	1	Ü
Consensus	Α	Ü	Ý	Â	Ğ	Δ	11		2

Nucleotide ^a		Mean CAT	% Mutant 30 S in		Thermodynamics ^d	
787	795	activity ^b	30 S peak ^c	70 S peaks	ΔG_{37}° (kcal/mol)	$T_{\rm m}$ (°C)
Α	С	100	46.1 ± 0.8	41.7 ± 3.3	-3.25	61.8
A	A C	83.8 ± 2.5	n.d.	n.d.	-2.90	61.3
<u>C</u>		80.5 ± 0.5	n.d.	n.d.	-2.84	60.7
<u>C</u>	<u>U</u>	74.1 ± 3.4	n.d.	n.d.	n.d.	n.d.
Α	טוטוטוט	72.1 ± 4.5	74.3 ± 0.5	14.3 ± 1.0	-5.62	75.3
<u>U</u>	<u>U</u>	72.0 ± 2.4	n.d.	n.d.	n.d.	n.d.
<u>G</u>	<u>U</u>	70.5 ± 1.8	56.1 ± 1.4	14.2 ± 0.6	-4.96	68.1
<u>U</u>	C	65.5 ± 2.1	n.d.	n.d.	-2.88	60.6
⊆	<u>A</u>	53.4 ± 1.0	n.d.	n.d.	n.d.	n.d.
<u>G</u>	<u>G</u>	52.9 ± 0.4	n.d.	n.d.	-3.70	64.9
$\underline{\mathbf{G}}$	<u>A</u>	46.0 ± 1.4	n.d.	n.d.	n.d.	n.d.
Α	<u>G</u>	37.5 ± 0.5	n.d.	n.d.	-3.19	63.5
<u>U</u>	<u>A</u>	36.7 ± 0.4	70.8 ± 7.4	10.1 ± 0.4	-5.82	74.3
<u>u</u>	AIGIAIGIAIGIO	13.5 ± 3.3	57.7 ± 12.1	5.5 ± 3.4	-5.15	69.4
א טוטוש טוטוטוטוטוש א טוטושוטוט		5.5 ± 1.8	58.3 ± 8.2	5.1 ± 1.3	-7.61	83.4
<u>C</u>	<u>G</u>	1.2 ± 0.1	n.d.	n.d.	n.d.	n.d.

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GACGCCGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACT TGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGT AAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAAC TTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACA ACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGA AGCCATACCAAACGACGAGCGTGACACCACGATGCCTGCAGCAATGGCAAC AACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAA CAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCT CGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCG TGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGT ATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAAT AGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAG ACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTT AAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTT AACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCTTAATAAGATGATCTTCT TGAGATCGTTTTGGTCTGCGCGTAATCTCTTGCTCTGAAAAACGAAAAAACCG CCTTGCAGGCCGTTTTTCGAAGGTTCTCTGAGCTACCAACTCTTTGAACCGA GGTAACTGGCTTGGAGGAGCGCAGTCACCAAAACTTGTCCTTTCAGTTTAGC CTTAACCGGCGCATGACTTCAAGACTAACTCCTCTAAATCAATTACCAGTGG CTGCTGCCAGTGGTGCTTTTGCATGTCTTTCCGGGTTGGACTCAAGACGATAG TTACCGGATAAGGCGCAGCGGTCGGACTGAACGGGGGGTTCGTGCATACAG TCCAGCTTGGAGCGAACTGCCTACCCGGAACTGAGTGTCAGGCGTGGAATGA GACAAACGCGGCCATAACAGCGGAATGACACCGGTAAACCGAAAGGCAGGA ACAGGAGAGCGCACGAGGGAGCCGCCAGGGGGAAACGCCTGGTATCTTTAT AGTCCTGTCGGGTTTCGCCACCACTGATTTGAGCGTCAGATTTCGTGATGCTT GTCAGGGGGGGGGCCTATGGAAAAACGGCTTTGCCGCGGCCCTCTCACTT CCCTGTTAAGTATCTTCCTGGCATCTTCCAGGAAATCTCCGCCCCGTTCGTAA GCCATTTCCGCTCGCCGCAGTCGAACGACCGAGCGTAGCGAGTCAGTGAGCG AGGAAGCGGAATATATCCTGTATCACATATTCTGCTGACGCACCGGTGCAGC CTTTTTCTCCTGCCACATGAAGCACTTCACTGACACCCTCATCAGTGCCAAC ATAGTAAGCCAGTATACACTCCGCTAGCATCGTCCATTCCGACAGCATCGCC AGTCACTATGGCGTGCTGCTAGCGCTATATGCGTTGATGCAATTTCTATGCGC ACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCCCCAGTCCTGCTCG CTTCGCTACTTGGAGCCACTATCGACTACGCGATCATGGCGACCACACCCGT CCTGTGGATCCTCTACGCCGGACGCATCGTGGCCGGCCACGATGCGTCCGGC GTAGAGGATCTATTTAACGACCCTGCCCTGAACCGACGACCGGGTCGAATTT GCTTTCGAATTTCTGCCATTCATCCGCTTATTATCACTTATTCAGGCGTAGCA CCAGGCGTTTAAGGGCACCAATAACTGCCTTAAAAAAATTACGCCCCGCCCT GCCACTCATCGCAGTACTGTTGTAATTCATTAAGCATTCTGCCGACATGGAA GCCATCACAGACGCATGATGAACCTGAATCGCCAGCGGCATCAGCACCTTG TCGCCTTGCGTATAATATTTGCCCATGGTGAAAACGGGGGCGAAGAAGTTGT CCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACCCAGGGATTGGC TGAGACGAAAAACATATTCTCAATAAACCCTTTAGGGAAATAGGCCAGGTTT TCACCGTAACACGCCACATCTTGCGAATATATGTGTAGAAACTGCCGGAAAT CGTCGTGGTATTCACTCCAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAA

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ACCCTGTTACCGCCGTGAAAGGGCGGTGTCCTGGGCCTCTAGACGAAGGGG ACACGAAAATTGCTTATCACGCGTTGCGTGATATTTTCGTGTAGGGTGAGCTT TCATTAATAGAAAGCGAACGGCCTTATTCTCTTCAGCCTCACTCCCAACGCGT AAACGCCTTGCTTTCACTTTCTATCAGACAATCTGTGTGAGCACTACAAAGT ACGCTTCTTTAAGGTAAGTGTGTGATCCAACCGCAGGTTCCCCTACGGTTACC TTGTTACGACTTCACCCCAGTCATGAATCACAAAGTGGTAAGCGCCCTCCCG AAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCG GTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCACGATTA CTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACG ACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCG CCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGATGACTTGACGT CATCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCC GGACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCC AACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACGGTT CCCGAAGGCACATTCTCATCTCTGAAAACTTCCGTGGATGTCAAGACCAGGT AAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGG GCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGT CGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAG TCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCC ACGCTTTCGCACCTGAGCGTCAGTCTTCGTCCAGGGGGCCGCCTTCGCCACC GGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCC CCTCTACGAGACTCAAGCTTGCCAGTATCAGATGCAGTTCCCAGGTTGAGCC TAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGA GTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATGAGCAAAGGTATTAACTT TACTCCCTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATA CACGCGCATGCCTCCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTG CTGCCTCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATC CTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTACT AGCTAATCCCATCTGGGCACATCCGATGGCAAGAGGCCCGAAGGTCCCCCTC TTTGGTCTTGCGACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCC CTCCATCAGGCAGTTTCCCAGACATTACTCACCCGTCCGCCACTCGTCAGCA AAGAAGCAAGCTTCTTCCTGTTACCGTTCGACTTGCATGTGTTAGGCCTGCCG CCAGCGTTCAATCTGAGCCATGATCAAACTCTTCAATTTAAAAGTTTGACGCT CAAAGAATTAAACTTCGTAATGAATTACGTGTTCACTCTTGAGACTTGGTATT CATTTTTCGTCTTGCGACGTTAAGAATCCGTATCTTCGAGTGCCCACACAGAT TGTCTGATAAATTGTTAAAGAGCAGTGCCGCTTCGCTTTTTCTCAGCGGCCGC TGTGTGAAATTGTTATCCGCTCACAATTCCACACATTATACGAGCCGGAAGC ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG CGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT TAATGAATCGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCCAG GGTGGTTTTCTTTTCACCAGTGAGACGGCCAACAGCTGATTGCCCTTCACCG CCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCTGGTTTGCCCCAGCAG GCGAAAATCCTGTTTGATGGTGGTTGACGGCGGGATATAACATGAGCTGTCT TCGGTATCGTCGTATCCCACTACCGAGATATCCGCACCAACGCGCAGCCCGG

ACTCGGTAATGGCGCCCATTGCGCCCAGCGCCATCTGATCGTTGGCAACCAG CATCGCAGTGGGAACGATGCCCTCATTCAGCATTTGCATGGTTTGTTGAAAA CCGGACATGGCACTCCAGTCGCCTTCCCGTTCCGCTATCGGCTGAATTTGATT GCGAGTGAGATATTTATGCCAGCCAGCCAGACGCAGACGCCGCGAGACAGA ACTTAATGGGCCCGCTAACAGCGCGATTTGCTGGTGACCCAATGCGACCAGA TGCTCCACGCCCAGTCGCGTACCGTCTTCATGGGAGAAAATAATACTGTTGA TGGGTGTCTGGTCAGAGACATCAAGAAATAACGCCGGAACATTAGTGCAGG CAGCTTCCACAGCAATGGCATCCTGGTCATCCAGCGGATAGTTAATGATCAG CCCACTGACCCGTTGCGCGAGAAGATTGTGCACCGCCGCTTTACAGGCTTCG ACGCCGCTTCGTTCTACCATCGACACCACCACGCTGGCACCCAGTTGATCGG CGCGAGATTTAATCGCCGCGACAATTTGCGACGGCGCGTGCAGGGCCAGACT GGAGGTGGCAACGCCAATCAGCAACGACTGTTTGCCCGCCAGTTGTTGTGCC ACGCGGTTGGGAATGTAATTCAGCTCCGCCATCGCCGCTTCCACTTTTTCCCG CGTTTTCGCAGAAACGTGGCTGGCCTGGTTCACCACGCGGGAAACGGTCTGA TAAGAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTCACAT TCACCACCCTGAATTGACTCTCTTCCGGGCGCTATCATGCCATACCGCGAAA GGTTTTGCACCATTCGATGGTGTCGGATCCTAGAGCGCACGAATGAGGGCCG ACAGGAAGCAAAGCTGAAAGGAATCAAATTTGGCCGCAGGCGTACCGTGGA CAGGAACGTCGTGCTGACGCTTCATCAGAAGGGCACTGGTGCAACGGAAATT GCTCATCAGCTCAGTATTGCCCGCTCCACGGTTTATAAAATTCTTGAAGACG AAAGGCCTCGTGCATACGCCTATTTTTATAGGTTAATGTCATGATAATAAT GGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCT ATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATA ACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAA CATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTT GCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGT GCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGA GTTTTCGCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTA TGTGGCGCGGTATTATCCCGTGTT

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CCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCT TAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAG GACCACTTCTGCGCTCGGCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCT GGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATG GTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTAT GGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCA TTCATTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATG ACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAG AAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGC AGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACC AAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCT GTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGC CAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG GATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGC TTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGA GAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGC **GGC**

AGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGG TATCTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT GTGATGCTCGTCAGGGGGGGGGGGGGCGAGCCTATGGAAAAACGCCAGCAACGCGGC CTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGC CCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAG CGGAAGAGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTCA CACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAA GCCAGTATACACTCCGCTATCGCTACGTGACTGGGTCATGGCTGCGCCCCGA CACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCAT CCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTT TTCACCGTCATCACCGAAACGCGCGAGGCAGCTGCGGTAAAGCTCATCAGCG TGGTCGTGAAGCGATTCACAGATGTCTGCCTGTTCATCCGCGTCCAGCTCGTT GAGTTTCTCCAGAAGCGTTAATGTCTGGCTTCTGATAAAGCGGGCCATGTTA AGGGCGGTTTTTTCCTGTTTGGTCACTTGATGCCTCCGTGTAAGGGGGAATTT CTGTTCATGGGGGTAATGATACCGATGAAACGAGAGGAGGATGCTCACGATA CGGGTTACTGATGATGAACATGCCCGGTTACTGGAACGTTGTGAGGGTAAAC AACTGGCGGTATGGATGCGGCGGGACCAGAGAAAAATCACTCAGGGTCAAT

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AAAAATGCACATGCTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCT TAGTGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGA GTGAAAAAGAACCTGAAACCGTGTACGTACAAGCAGTGGGAGCACGCTTAG GCGTGTGACTGCGTACCTTTTGTATAATGGGTCAGCGACTTATATTCTGTAGC AAGGTTAACCGAATAGGGGAGCCGAAGGGAAACCGAGTCTTAACTGGGCGT TAAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGTTG AAGGTTGGGTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAAATT AGCGGATGACTTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGATAGC TGGTTCTCCCGAAAGCTATTTAGGTAGCGCCTCGTGAATTCATCTCCGGGG GTAGAGCACTGTTTCGGCAAGGGGGTCATCCCGACTTACCAACCCGATGCAA ACTGCGAATACCGGAGAATGTTATCACGGGAGACACACGGCGGGTGCTAAC GTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAGGTCCCAAAGT CATGGTTAAGTGGGAAACGATGTGGGAAGGCCCAGACAGCCAGGATGTTGG CTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTCACTGGTCGAGTCG GCCTGCGCGGAAGATGTAACGGGGCTAAACCATGCACCGAAGCTGCGGCAG CGACGCTTATGCGTTGTTGGGTAGGGGAGCGTTCTGTAAGCCTGCGAAGGTG TGCTGTGAGGCATGCTGGAGGTATCAGAAGTGCGAATGCTGACATAAGTAAC GATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAGACCAAGGGTTCCTGTCCA ACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGCCGAAAGGCGT AGTCGATGGGAAACAGGTTAATATTCCTGTACTTGGTGTTACTGCGAAGGGG GGACGGAGAAGGCTATGTTGGCCGGGCGACGGTTGTCCCGGTTTAAGCGTGT AGGCTGGTTTTCCAGGCAAATCCGGAAAATCAAGGCTGAGGCGTGATGACG AGGCACTACGGTGCTGAAGCAACAAATGCCCTGCTTCCAGGAAAAGCCTCTA AGCATCAGGTAACATCAAATCGTACCCCAAACCGACACAGGTGGTCAGGTA GAGAATACCAAGGCGCTTGAGAGAACTCGGGTGAAGGAACTAGGCAAAATG GTGCCGTAACTTCGGGAGAAGGCACGCTGATATGTAGGTGAGGTCCCTCGCG GATGGAGCTGAAATCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTAAA AACACAGCACTGTGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGC CCGGTGCCGGAAGGTTAATTGATGGGGTTAGCGCAAGCGAAGCTCTTGATCG AAGCCCCGGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAAT TCCTTGTCGGGTAAGTTCCGACCTGCACGAATGGCGTAATGATGGCCAGGCT GTCTCCACCCGAGACTCAGTGAAATTGAACTCGCTGTGAAGATGCAGTGTAC CCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACTGAA CATTGAGCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGTGTGGACGCCA GTCTGCATGGAGCCGACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAAC GTTGACCCGTAATCCGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGG GCGGTCTCCTAAAGAGTAACGGAGGAGCACGAAGGTTGGCTAATCCTGG TCGGACATCAGGAGGTTAGTGCAATGGCATAAGCCAGCTTGACTGCGAGCGT GACGCCGCGAGCAGGTCCGAAAGCAGGTCATAGTGATCCGGTGGTTCTGAA TGGAAGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAACAGGCTG ATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCGATGTCGGC TCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCCATT TAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGTCCCTA TCTGCCGTGGGCGCTGGAGAACTGAGGGGGGCTGCTCCTAGTACGAGAGGA

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CAGGAGAGCGTTCACCGACAAACAACAGATAAAACGAAAGGCCCAGTCTTT CGACTGAGCCTTTCGTTTTATTTGATGCCTGGCAGTTCCCTACTCTCGCATGG GGAGACCCCACACTACCATCGGCGCTACGACTAGATTATTTGTAGAGCTCAT CCATGCCATGTGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTG GTCACGCTTTTCGTTGGGATCTTTCGAAAGGGCAGATTGTGTCGACAGGTAA TGGTTGTCTGGTAAAAGGACAGGGCCATCGCCAATTGGAGTATTTTGTTGAT AATGGTCTGCTAGTTGAACGGATCCATCTTCAATGTTGTGGCGAATTTTGAA GTTAGCTTTGATTCCATTCTTTTGTTTGTCTGCCGTGATGTATACATTGTGTGA GTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTAAAAT CAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACTTGACT TCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTG TACATAACCTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGA TCCGGATAACGGGAAAAGCATTGAACACCATAAGAGAAAGTAGTGACAAGT GCTTTCCGTATGTAGCATCACCTTCACCCTCTCCACTGACAGAAAATTTGTGC CCATTAACATCACCATCTAATTCAACAAGAATTGGGACAACTCCAGTGAAAA GTTCTTCTCCTTTGCTCGCAGTGATTTTTTTTCTCCATTTGCGGAGGGATATGA AAGCGGCCGCTTCCACACATTAAACTAGTTCGATGATTAATTGTCAACAGCT CGCCGGCGCACCTCGCTAACGGATTCACCACTCCAAGAATTGGAGCCAATC GATTCTTGCGGAGAACTGTGAATGCGGGTACCCAGATCCGGAACATAATGGT GCAGGGCGCTGACTTCCGCGTTTCCAGACTTTACGAAACACGGAAACCGAAG ACCATTCATGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGTCGCTTCA CGTTCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACCCCGC CAGCCTAGCCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCC AGGACCCAACGCTGCCGAGATGCGCCGCGTGCGGCTGCTGGAGATGGCGG ACGCGATGGATATGTTCTGCCAAGGGTTGGTTTGCGCATTCACAGTTCTCCGC AAGAATCGATTGGCTCCAATTCTTGGAGTGGTGAATCCGTTAGCGAGGTGCC GCCGGCGAGCTGTTGACAATTAATCATCGAACTAGTTTAATGTGTGGAAGCG GCCGCTTTCATATCCCTCCGCAAATGGAGAAAAAAATCACTGGATATACCAC CGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCAGTCA GTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTT AAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATT CTTGCCCGCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACG GTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAG CAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGC AGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGC CTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCT GGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTC GCCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGA TGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGC AGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCG TAATTTTTTAAGGCAGTTATTGGTGCCCTTAAACGCCTGGTGCTACGCCTGA ATAAGTGATAATAAGCGGATGAATGGCAGAAATTCGAAAGCAAATTCGACC CGGTCGTCGGTCAGGGCAGGGTCGTTAAATAGCCGCTTATGTCTATTGCTG GTTTACGGTTTATTGACTACCCGAAGCAGTGTGACCCTGTGCTTCTCAAATGC

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